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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/086,814

DATE: 10/30/2002 PG
TIME: 13:57:57

Input Set : A:\61010AB1.ST25.txt
Output Set: N:\CRF4\10302002\J086814.raw

3 <110> APPLICANT: Dragic, Tatjana
4 Olson, William C.
6 <120> TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
8 <130> FILE REFERENCE: 61010-AB-1
10 <140> CURRENT APPLICATION NUMBER: US 10/086,814
11 <141> CURRENT FILING DATE: 2002-02-28
13 <160> NUMBER OF SEQ ID NOS: 38
15 <170> SOFTWARE: PatentIn version 3.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 352
19 <212> TYPE: PRT
20 <213> ORGANISM: Homo sapiens
22 <400> SEQUENCE: 1
24 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
25 1 5 10 15
28 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
29 20 25 30
32 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
33 35 40 45
36 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
37 50 55 60
40 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
41 65 70 75 80
44 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
45 85 90 95
48 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
49 100 105 110
52 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
53 115 120 125
56 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
57 130 135 140
60 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
61 145 150 155 160
64 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
65 165 170 175
68 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
69 180 185 190
72 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
73 195 200 205
76 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
77 210 215 220
80 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
81 225 230 235 240

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84 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
85 245 250 255
88 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
89 260 265 270
92 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
93 275 280 285
96 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
97 290 295 300
100 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
101 305 310 315 320
104 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
105 325 330 335
108 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
109 340 345 350
112 <210> SEQ ID NO: 2
113 <211> LENGTH: 1376
114 <212> TYPE: DNA
115 <213> ORGANISM: Homo sapiens
117 <400> SEQUENCE: 2
118 gaattcccccc aacagagcca agctctccat ctatggaca gggaaagctag cagcaaacct 60
120 tcccttcact acaaaaacttc attgcttgc caaaaaagaga gtttaattcaa tgttagacatc 120
122 tatgttaggca attaaaaacc tatttgatgta taaaacagt tgcattcatg gaggcaact 180
124 aaatacattc taggacttta taaaagatca ctttttatgg atgcacaggg tggaacaaga 240
126 tggatttatca agtgtcaagt ccaatctatg acatcaatta ttatacatcg gagccctgcc 300
128 aaaaaatcaa tgtgaagcaa atcgcagccc gcctcctgcc tccgctctac tcactggtgt 360
130 tcatactttgg ttttggggc aacatgctgg tcatacctcat cctgataaac tgcaaaaggc 420
132 tgaagagcat gactgacatc tacctgctca acctggccat ctctgacctg ttttccttc 480
134 ttactgtccc cttctggct cactatgctg ccgcggcgtg ggactttgga aatacaatgt 540
136 gtcaactctt gacagggtctc tattttatacg gtttcttc tggaatcttc ttcatcatcc 600
138 tcctgacaat cgataggtac ctggctgtcg tccatgctgt gtttgcattt aaagccagga 660
140 cggtcaccc tgggggtggta acaagtgtga tcacttgggt ggtggctgtg tttgcgtctc 720
142 tcccaggaat catcttacc agatctcaa aagaaggctc tcattacacc tgcaagctctc 780
144 atttccata cagtcagttt caattctgaa agaatttcca gacattaaag atagtcatct 840
146 tggggctggg cctgcgtcg cttgtcatgg tcatactgcta ctgcggaaatc ctaaaaactc 900
148 tgcttcgggt tcgaaatgag aagaagaggc acagggtctg gaggcttatac ttcaccatca 960
150 tgattgttta ttttctcttc tggggctccct acaacattgt ctttcctcg aacacccctcc 1020
152 aggaattctt tggcctgaat aattgcagta gctctaacag gttggaccaa gctatgcagg 1080
154 tgacagagac tcttggatg acgcactgt gcatcaaccc catcatctat gccttgcgtcg 1140
156 gggagaagtt cagaaactac ctcttagtct ttttccaaaa gcacattgcc aaacgcttct 1200
158 gcaaattgtcg ttctattttc cagcaagagg ctcccgagcg agcaagctca gtttacaccc 1260
160 gatccactgg ggagcaggaa atatctgtgg gtttgcata gggactcaag tgggtgggt 1320
162 acccagtcag agttgtgcac atggcttagt ttctatacac agcctgggt ggggt 1376
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 12
167 <212> TYPE: PRT
168 <213> ORGANISM: Homo sapiens
170 <220> FEATURE:
171 <221> NAME/KEY: MISC_FEATURE
172 <222> LOCATION: (1)..(1)

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Input Set : A:\61010AB1.ST25.txt
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173 <223> OTHER INFORMATION: Any amino acid
 176 <220> FEATURE:
 177 <221> NAME/KEY: MISC_FEATURE
 178 <222> LOCATION: (2)..(2)
 179 <223> OTHER INFORMATION: Xaa represents from 0 to 9 amino acids, where if there are
 more t
 180 than 2 amino acids, they have a sequence identical to the sequence
 181 set forth in SEQ ID NO: 1 beginning with the Ile at position 9 a
 182 nd extending therefrom in the amino terminal direction.
 185 <220> FEATURE:
 186 <221> NAME/KEY: MOD_RES
 187 <222> LOCATION: (3)..(3)
 188 <223> OTHER INFORMATION: SULFATATION
 191 <220> FEATURE:
 192 <221> NAME/KEY: MOD_RES
 193 <222> LOCATION: (7)..(7)
 194 <223> OTHER INFORMATION: SULFATATION
 197 <220> FEATURE:
 198 <221> NAME/KEY: MISC_FEATURE
 199 <222> LOCATION: (11)..(11)
 200 <223> OTHER INFORMATION: Xaa represents from 0 to 14 amino acids, where if there are
 more t
 201 than 2 amino acids, they have a sequence identical to the sequenc
 202 e set forth in SEQ ID NO: 1 beginning with the Glu at position 18
 203 and extending therefrom in the carboxy terminal direction.
 206 <220> FEATURE:
 207 <221> NAME/KEY: MISC_FEATURE
 208 <222> LOCATION: (12)..(12)
 209 <223> OTHER INFORMATION: Any amino acid
 212 <400> SEQUENCE: 3
 W--> 214 Xaa Xaa Tyr Asp Ile Asn Tyr Tyr Thr Ser Xaa Xaa
 215 1 5 10
 218 <210> SEQ ID NO: 4
 219 <211> LENGTH: 12
 220 <212> TYPE: PRT
 221 <213> ORGANISM: Homo sapiens
 223 <220> FEATURE:
 224 <221> NAME/KEY: MISC_FEATURE
 225 <222> LOCATION: (2)..(2)
 226 <223> OTHER INFORMATION: Xaa represents from 0 to 9 amino acids, where if there are
 more t
 227 than 2 amino acids, they have a sequence identical to the sequence
 228 set forth in SEQ ID NO: 1 beginning with the Ile at position 9 a
 229 nd extending therefrom in the amino terminal direction.
 232 <220> FEATURE:
 233 <221> NAME/KEY: MISC_FEATURE
 234 <222> LOCATION: (1)..(1)
 235 <223> OTHER INFORMATION: Xaa is any amino acid
 238 <220> FEATURE:
 239 <221> NAME/KEY: MOD_RES
 240 <222> LOCATION: (7)..(8)
 241 <223> OTHER INFORMATION: SULFATATION

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Input Set : A:\61010AB1.ST25.txt

Output Set: N:\CRF4\10302002\J086814.raw

244 <220> FEATURE:
 245 <221> NAME/KEY: MISC_FEATURE
 246 <222> LOCATION: (11)..(11)
 247 <223> OTHER INFORMATION: Xaa represents from 0 to 14 amino acids, where if there are
 more
 248 than 2 amino acids, they have a sequence identical to the sequenc
 249 e set forth in SEQ ID NO: 1 beginning with the Glu at position 18
 250 and extending therefrom in the carboxy terminal direction.
 253 <220> FEATURE:
 254 <221> NAME/KEY: MISC_FEATURE
 255 <222> LOCATION: (12)..(12)
 256 <223> OTHER INFORMATION: Xaa is any amino acid
 259 <400> SEQUENCE: 4
 W--> 261 Xaa Xaa Tyr Asp Ile Asn Tyr Tyr Thr Ser Xaa Xaa
 262 1 5 10
 265 <210> SEQ ID NO: 5
 266 <211> LENGTH: 12
 267 <212> TYPE: PRT
 268 <213> ORGANISM: Homo sapiens
 270 <220> FEATURE:
 271 <221> NAME/KEY: MISC_FEATURE
 272 <222> LOCATION: (1)..(1)
 273 <223> OTHER INFORMATION: Xaa is any amino acid
 276 <220> FEATURE:
 277 <221> NAME/KEY: MISC_FEATURE
 278 <222> LOCATION: (2)..(2)
 279 <223> OTHER INFORMATION: Xaa represents from 0 to 9 amino acids, where if there are
 more t
 280 han 2 amino acids, they have a sequence identical to the sequence
 281 set forth in SEQ ID NO: 1 beginning with the Ile at position 9 a
 282 nd extending therefrom in the amino terminal direction.
 285 <220> FEATURE:
 286 <221> NAME/KEY: MOD_RES
 287 <222> LOCATION: (3)..(3)
 288 <223> OTHER INFORMATION: SULFATATION
 291 <220> FEATURE:
 292 <221> NAME/KEY: MOD_RES
 293 <222> LOCATION: (8)..(8)
 294 <223> OTHER INFORMATION: SULFATATION
 297 <220> FEATURE:
 298 <221> NAME/KEY: MISC_FEATURE
 299 <222> LOCATION: (11)..(11)
 300 <223> OTHER INFORMATION: Xaa represents from 0 to 14 amino acids, where if there are
 more
 301 than 2 amino acids, they have a sequence identical to the sequenc
 302 e set forth in SEQ ID NO: 1 beginning with the Glu at position 18
 303 and extending therefrom in the carboxy terminal direction.
 306 <220> FEATURE:
 307 <221> NAME/KEY: MISC_FEATURE
 308 <222> LOCATION: (12)..(12)
 309 <223> OTHER INFORMATION: Xaa is any amino acid
 312 <400> SEQUENCE: 5

RAW SEQUENCE LISTING
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Input Set : A:\61010AB1.ST25.txt
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W--> 314 Xaa Xaa Tyr Asp Ile Asn Tyr Tyr Thr Ser Xaa Xaa
 315 1 5 10
 318 <210> SEQ ID NO: 6
 319 <211> LENGTH: 12
 320 <212> TYPE: PRT
 321 <213> ORGANISM: Homo sapiens
 323 <220> FEATURE:
 324 <221> NAME/KEY: MISC_FEATURE
 325 <222> LOCATION: (1)..(1)
 326 <223> OTHER INFORMATION: Xaa is any amino acid
 329 <220> FEATURE:
 330 <221> NAME/KEY: MOD_RES
 331 <222> LOCATION: (1)..(1)
 332 <223> OTHER INFORMATION: ACETYLATION
 335 <220> FEATURE:
 336 <221> NAME/KEY: MISC_FEATURE
 337 <222> LOCATION: (2)..(2)
 338 <223> OTHER INFORMATION: Xaa represents from 0 to 9 amino acids, where if there are
 more t
 339 han 2 amino acids, they have a sequence identical to the sequence
 340 set forth in SEQ ID NO: 1 beginning with the Ile at position 9 a
 341 nd extending therefrom in the amino terminal direction.
 344 <220> FEATURE:
 345 <221> NAME/KEY: MOD_RES
 346 <222> LOCATION: (3)..(3)
 347 <223> OTHER INFORMATION: SULFATATION
 350 <220> FEATURE:
 351 <221> NAME/KEY: MOD_RES
 352 <222> LOCATION: (7)..(7)
 353 <223> OTHER INFORMATION: SULFATATION
 356 <220> FEATURE:
 357 <221> NAME/KEY: MISC_FEATURE
 358 <222> LOCATION: (11)..(11)
 359 <223> OTHER INFORMATION: Xaa represents from 0 to 14 amino acids, where if there are
 more
 360 than 2 amino acids, they have a sequence identical to the sequenc
 361 e set forth in SEQ ID NO: 1 beginning with the Glu at position 18
 362 and extending therefrom in the carboxy terminal direction.
 365 <220> FEATURE:
 366 <221> NAME/KEY: MISC_FEATURE
 367 <222> LOCATION: (12)..(12)
 368 <223> OTHER INFORMATION: Xaa is any amino acid
 371 <400> SEQUENCE: 6
 W--> 373 Xaa Xaa Tyr Asp Ile Asn Tyr Tyr Thr Ser Xaa Xaa
 374 1 5 10
 377 <210> SEQ ID NO: 7
 378 <211> LENGTH: 12
 379 <212> TYPE: PRT
 380 <213> ORGANISM: Homo sapiens
 382 <220> FEATURE:
 383 <221> NAME/KEY: MISC_FEATURE

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/086,814

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Input Set : A:\61010AB1.ST25.txt
Output Set: N:\CRF4\10302002\J086814.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 1,2,11,12
Seq#:4; Xaa Pos. 1,2,11,12
Seq#:5; Xaa Pos. 1,2,11,12
Seq#:6; Xaa Pos. 1,2,11,12
Seq#:7; Xaa Pos. 1,2,11,12
Seq#:8; Xaa Pos. 1,2,11,12
Seq#:9; Xaa Pos. 1,2,11,12
Seq#:10; Xaa Pos. 1,2,11,12
Seq#:11; Xaa Pos. 1,2,11,12
Seq#:12; Xaa Pos. 1,2,11,12
Seq#:13; Xaa Pos. 1,2,11,12
Seq#:14; Xaa Pos. 1,2,11,12
Seq#:15; Xaa Pos. 1,2,11,12
Seq#:16; Xaa Pos. 1,2,11,12
Seq#:17; Xaa Pos. 1,2,11,12
Seq#:18; Xaa Pos. 1,2,11,12
Seq#:19; Xaa Pos. 1,2,11,12
Seq#:20; Xaa Pos. 1,2,11,12
Seq#:21; Xaa Pos. 1,2,11,12
Seq#:22; Xaa Pos. 1,2,11,12
Seq#:23; Xaa Pos. 1,2,11,12
Seq#:24; Xaa Pos. 1,2,11,12
Seq#:25; Xaa Pos. 1,2,11,12
Seq#:26; Xaa Pos. 1,2,11,12

VERIFICATION SUMMARY
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Input Set : A:\61010AB1.ST25.txt
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L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:544 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:898 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:945 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:998 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:1057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:1110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:1169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:1281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:1340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:1405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:1464 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:1529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0